OM protein - protein search, using sw model

Run on: September 16, 2005, 08:30:51 ; Search time 30.5 seconds

GenCore version 5.1.6
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(without alignment)
974.109 Million cell updates/sec

Title: US-10-643-627-6
Perfect score: 398
Sequence: 1 MNVLSFEQTSVTAETFISVM.........KHSRKSSSYSSSSTTVKTSY 398

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptcdata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	398	100.0	398	3	US-08-486-673B-6	Sequence 6, Appli
2	291	73.1	398	1	US-08-097-938-6	Sequence 6, Appli
3	291	73.1	398	1	US-08-476-000-6	Sequence 6, Appli
4	291	73.1	398	2	US-08-472-840-6	Sequence 6, Appli
5	291	73.1	398	3	US-08-476-976-6	Sequence 6, Appli
6	291	73.1	398	3	US-08-474-410-6	Sequence 6, Appli
7	217	54.5	398	1	US-08-097-938-4	Sequence 4, Appl
8	217	54.5	398	1	US-08-476-000-4	Sequence 4, Appli
9	217	54.5	398	1	US-08-472-840-4	Sequence 4, Appli
10	217	54.5	398	3	US-08-476-976-4	Sequence 4, Appli
11	217	54.5	398	3	US-08-474-410-4	Sequence 4, Appli
12	217	54.5	398	3	US-08-486-673B-4	Sequence 4, Appli
13	155	38.9	394	2	US-08-742-440A-8	Sequence 8, Appli
14	114	28.6	397	1	US-08-486-673B-63	Sequence 63, Appl
15	91	22.9	397	1	US-08-476-000-63	Sequence 63, Appl
16	91	22.9	397	2	US-08-472-840-63	Sequence 63, Appl
17	91	22.9	397	3	US-08-476-976-63	Sequence 63, Appli
18	91	22.9	397	3	US-08-474-410-63	Sequence 63, Appl
19	34	8.5	395	1	US-08-097-938-2	Sequence 2, Appl
20	34	8.5	395	1	US-08-476-000-2	Sequence 2, Appli
21	34	8.5	395	1	US-08-472-840-2	Sequence 2, Appl
22	34	8.5	395	1	US-08-476-976-2	Sequence 2, Appli
23	34	8.5	395	1	US-08-474-410-2	Sequence 2, Appli
24	34	8.5	395	1	US-08-472-840-5	Sequence 5, Appli
25	34	8.5	395	2	US-08-476-976-2	Sequence 2, Appl
26	34	8.5	395	2	US-08-472-840-2	Sequence 5, Appl
27	34	8.5	395	3	US-08-474-410-2	Sequence 5, Appli
28	34	8.5	395	3	US-08-474-410-5	Sequence 5, Appli
29	34	8.5	395	3	US-08-486-673B-2	Sequence 2, Appli
30	34	8.5	395	3	US-08-486-673B-5	Sequence 61, Appl
31	34	8.5	399	1	US-08-472-840-61	Sequence 61, Appli
32	34	8.5	399	2	US-08-476-976-61	Sequence 61, Appli
33	34	8.5	399	3	US-08-474-410-61	Sequence 61, Appl
34	34	8.5	399	3	US-08-476-976-61	Sequence 61, Appli
35	34	8.5	399	3	US-08-486-673B-21	Sequence 21, Appli
36	22	5.5	25	4	US-09-472-130A-19	Sequence 19, Appl
37	15	3.8	31	1	US-08-097-938-21	Sequence 21, Appl
38	15	3.8	31	1	US-08-476-000-21	Sequence 21, Appli
39	15	3.8	31	1	US-08-472-840-21	Sequence 21, Appli
40	15	3.8	31	2	US-08-476-976-21	Sequence 21, Appli
41	15	3.8	31	3	US-08-474-410-21	Sequence 21, Appli
42	13	2.5	13	1	US-08-097-938-41	Sequence 41, Appl
43	13	2.5	13	1	US-08-476-000-41	Sequence 41, Appli
44	13	2.5	13	1	US-08-472-840-41	Sequence 41, Appl
45	13	2.5	13	2	US-08-476-976-41	Sequence 41, Appli
46	13	2.5	13	3	US-08-474-410-41	Sequence 41, Appli
47	13	2.5	13	3	US-08-474-410-41	Sequence 41, Appl
48	13	2.5	26	1	US-07-657-769B-42	Sequence 42, Appl
49	10	2.5	26	1	US-07-789-184-103	Sequence 103, Appl
50	10	2.5	26	1	US-07-789-184-214	Sequence 214, App
51	10	2.5	26	1	US-07-789-184-217	Sequence 217, App
52	10	2.5	26	1	US-08-476-000-217	Sequence 217, Appl
53	10	2.5	26	2	US-08-477-362-103	Sequence 103, App
54	10	2.5	26	2	US-08-475-263-214	Sequence 214, Appl
55	10	2.5	26	2	US-08-475-263-217	Sequence 217, App
56	10	2.5	26	1	US-08-475-263-217	Sequence 217, Appl
57	10	2.5	26	1	US-07-789-184-103	Sequence 103, App
58	10	2.5	26	1	US-08-485-886-217	Sequence 217, App
59	10	2.5	26	1	US-08-477-362-103	Sequence 103, App
60	10	2.5	26	2	US-08-477-362-214	Sequence 214, App
61	10	2.5	26	2	US-08-477-362-217	Sequence 217, Appl
62	10	2.5	26	2	US-08-477-134-103	Sequence 103, App
63	10	2.5	26	2	US-08-477-134-214	Sequence 214, Appl
64	10	2.5	26	2	US-08-477-134-217	Sequence 217, App
65	10	2.5	26	1	US-08-473-489A-103	Sequence 103, App
66	10	2.5	26	3	US-08-473-489A-214	Sequence 214, App
67	10	2.5	26	3	US-08-473-489A-217	Sequence 217, Appl
68	10	2.5	26	3	US-08-485-695-103	Sequence 103, App
69	10	2.5	26	3	US-08-485-695-214	Sequence 214, App
70	10	2.5	26	3	US-08-485-695-217	Sequence 217, App
71	10	2.5	26	3	US-08-018-760-103	Sequence 103, App
72	10	2.5	26	3	US-08-018-760-214	Sequence 214, App
73	10	2.5	26	3	US-08-018-760-217	Sequence 217, Appl
74	10	2.5	408	2	US-08-742-440A-6	Sequence 6, Appli
75	10	2.5	425	1	US-07-657-769B-69	Sequence 69, Appli
76	10	2.5	425	1	US-08-097-938-7	Sequence 7, Appli
77	10	2.5	425	2	US-07-789-184-220	Sequence 220, Appl
78	10	2.5	425	2	US-08-311-553-13	Sequence 13, Appl
79	10	2.5	425	1	US-07-789-184-220	Sequence 220, App
80	10	2.5	425	1	US-08-476-000-7	Sequence 7, Appli
81	10	2.5	425	1	US-08-477-263-220	Sequence 220, App
82	10	2.5	425	1	US-08-472-840-7	Sequence 7, Appl
83	10	2.5	425	1	US-08-477-362-220	Sequence 220, App
84	10	2.5	425	1	US-08-477-134-220	Sequence 220, App
85	10	2.5	425	2	US-08-476-976-7	Sequence 7, Appli
86	10	2.5	425	2	US-08-911-320A-3	Sequence 3, Appli
87	10	2.5	425	2	US-08-476-976-7	Sequence 7, Appli
88	10	2.5	425	3	US-08-473-489A-220	Sequence 220, Appl
89	10	2.5	425	3	US-08-560-098A-57	Sequence 57, Appl
90	10	2.5	425	3	US-08-767-993-13	Sequence 13, Appli
91	10	2.5	425	3	US-08-474-410-7	Sequence 7, Appli
92	10	2.5	425	3	US-08-485-695-220	Sequence 220, App
93	10	2.5	425	3	US-09-217-101-3	Sequence 3, Appl
94	10	2.5	425	3	US-08-018-760-220	Sequence 220, App
95	10	2.5	425	4	US-08-486-673B-7	Sequence 7, Appli
96	10	2.3	12	1	US-09-054-272-53	Sequence 53, Appli
97	9	2.3	12	1	US-08-097-938-42	Sequence 42, Appl
98	9	2.3	12	2	US-08-476-976-42	Sequence 42, Appl
99	9	2.3	12	2	US-08-472-840-42	Sequence 42, Appl
100	9	2.3	12	3	US-08-476-976-42	Sequence 42, Appl

```
QM protein - protein search, using sw model

Run on:        September 16, 2005, 08:17:59 ; Search time 119.5 Seconds
                                             (without alignments)
                                             1288.122 Million cell updates/sec

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               GenCore version 5.1.6

Title:         US-10-643-627-6
Perfect score: 398
Sequence:      1 MNVLSFEOTSVTAETPISVM.......KHSRKSSSYSSSSTTVKTSY 398
Scoring table: 1
Searched:      2105692 seqs, 386760381 residues
Word size :    0
Total number of hits satisfying chosen parameters:       2105692
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Listing first 1000 summaries

Database :   A_Geneseq_16Dec04:*
          1: geneseqp1908:*
          2: geneseqp1990s:*
          3: geneseqp2000s:*
          4: geneseqp2001s:*
          5: geneseqp2002s:*
          6: geneseqp2003aa:*
          7: geneseqp2003bs:*
          8: geneseqp2004s:*

          OLIGO Gapop 60.0 , Gapext 60.0

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	%	Query Match Length	DB	ID	Description
1	217	54.5	397	3	AAB35641	Human PAR
2	217	54.5	397	5	AAE26678	Human coa
3	217	54.5	397	5	ABG73508	Human par
4	217	54.5	397	7	ADE62812	Human Pro
5	217	54.5	397	8	ADL61221	Human coa
6	217	54.5	397	8	ADO29311	Human GPC
7	217	54.5	397	8	ADS74020	Human G-p
8	217	54.5	398	2	AAR66921	Human C14
9	217	54.5	398	2	AAW01953	Human C14
10	162	40.7	320	8	ADI28655	Human mod
11	162	40.7	341	8	ADI28654	Human mod
12	162	40.7	355	6	ADI28653	Human mod
13	162	40.7	397	6	ABP81907	Human pro
14	162	40.7	397	7	ADK52594	Hematolog
15	162	40.7	397	7	ADN39997	Cancer/an
16	162	40.7	394	2	ADR46675	Cancer-as
17	155	38.9	397	8	AAW51408	Human pro
18	91	22.9	397	2	AAR66923	Human C14
19	91	22.9	397	2	AAW01955	Human C14
20	57	14.3	389	8	ADO28601	Human PAR
21	37	9.3	397	7	ADE62810	Rat Prote
22	37	9.3	397	7	ABU67239	G-protein
23	35	8.8	58	5	ABP54020	Human pro
24	35	8.8	58	8	ADO28760	Human pro
25	35	8.8	58	8	ADO05264	Proteinas
26	34	8.5	395	2	AAR66920	Murine C1
27	34	8.5	395	2	AAW01952	Murine C1
28	34	8.5	399	2	AAR66922	Murine C1
29	34	8.5	399	2	AAW01954	Murine C1
30	34	8.5	399	7	ABR63562	Delayed h
31	34	8.5	399	8	ADO29312	Mouse GPC
32	25	6.3	54	8	ADI28666	Human pro
33	22	5.5	399	3	AAY45037	Human pro
34	21	5.3	399	2	AAU10420	PAR2 pepd
35	20	5.0	399	2	AAU10421	PAR2 pepd
36	19	4.8	20	6	ABP82705	G protein
37	18	4.5	18	6	ABP82706	G protein
38	15	3.8	68	6	ABP82707	G protein
39	14	3.5	20	8	ADK35286	Novel hum
40	12	3.0	12	3	ABG35651	Human PAR
41	12	3.0	16	6	AAW76406	Human PAR
42	11	2.8	20	3	ABP82708	G protein
43	10	2.5	13	2	AAB35652	Mouse PAR
44	10	2.5	13	2	AAR66890	Agonist P
45	10	2.5	15	5	AAW01923	C140 rece
46	10	2.5	15	5	ABG35286	Human PAR
47	10	2.5	15	5	ABG35288	Human PAR
48	10	2.5	15	5	ABG35287	Human PAR
49	10	2.5	15	5	ABG35289	Human PAR
50	10	2.5	26	2	ABG35285	Human PAR
51	10	2.5	15	2	AAR27238	Thrombin
52	10	2.5	319	4	AAB27760	Rat G-pro
53	10	2.5	319	2	ADO29401	Mouse GPC
54	10	2.5	371	5	AAW51406	Human PAR
55	10	2.5	374	2	ABG73509	Human par
56	10	2.5	374	5	ABP81908	Human pro
57	10	2.5	374	6	ADB67661	F2R
58	10	2.5	374	7	ADO29313	Human GPC
59	10	2.5	374	8	ADQ97469	Human can
60	10	2.5	374	8	ADQ39889	Human myo
61	10	2.5	374	8	ADS32990	Proteinas
62	10	2.5	374	8	ABG35298	Human PAR
63	10	2.5	402	5	AAR27240	Human thr
64	10	2.5	425	2	AAR60698	Fragment
65	10	2.5	425	2	AAW51407	Human pro
66	10	2.5	425	2	AAY49570	Human thr
67	10	2.5	425	2	AAE17032	Human thr
68	10	2.5	425	5	ABG35300	Human PAR
69	10	2.5	425	5	AAG80697	Human PAR
70	10	2.5	425	5	ABG73511	Human thr
71	10	2.5	425	6	ABR47449	Breast ca
72	10	2.5	425	6	ABP81919	Human thr
73	10	2.5	425	7	ADE58075	Human pro
74	10	2.5	425	7	ADE58071	Human Pro
75	10	2.5	425	7	ADG89876	Human coa
76	10	2.5	425	7	ADL14208	Novel hum
77	10	2.5	425	8	ADN04016	Antipsori
78	10	2.5	425	8	ADO29309	Human GPC
79	10	2.5	425	8	ADQ18985	Human sof
80	10	2.5	425	8	ADR45608	Human G p
81	10	2.5	425	8	ADS04489	Human pro
82	10	2.5	425	3	AAY45035	Human pro
83	10	2.5	425	8	ADO29310	Mouse GPC
84	10	2.5	426	3	ADE58073	Rat Prote
85	10	2.5	430	8	ADE58069	Human thr
86	10	2.5	432	7	AAW16314	Human thr
87	10	2.5	892	2	AAR66891	Agonist P
88	9	2.3	12	2	ABG35284	C140 rece
89	9	2.3	15	5	AAW01924	C140 rece
90	9	2.3	15	5	AAW76405	Human PAR
91	9	2.3	17	4	ABM37814	Propionib
92	9	2.3	137	6	AAU41295	Propionib
93	9	2.3	137	6	ABM37814	Propionib
94	9	2.3	8	8	ADP49257	Disease-a
95	8	2.0	11	2	AAR66892	Agonist p
96	8	2.0	11	2	AAW01925	C140 rece
97	8	2.0	15	5	ABG35283	Human PAR
98	8	2.0	20	2	AAW76404	Rat PAR-2

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: September 16, 2005, 08:21:20 ; Search time 26 Seconds
(without alignments)
1472.857 Million cell updates/sec

Title: US-10-643-627-4
Perfect score: 398
Sequence: 1 MNVLSPEQSVTAETPISVM..........KHSRKSSSYSSSSTTVKTSY 398
Scoring table: OLIGO
                  Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 9621676763 residues

Word size :   0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :   PIR_79:*
                  1: pir1:*
                  2: pir2:*
                  3: pir3:*
                  4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	370	93.0	397	2	S66518	proteinase-activat
2	34	8.5	399	2	I48705	proteinase activat
3	10	2.5	425	2	A37912	thrombin receptor
4	10	2.5	427	2	S17148	alpha-thrombin rec
5	10	2.5	432	2	A43448	thrombin receptor
6	8	2.0	239	2	T21050	thrombin receptor
7	8	2.0	244	2	B86197	hypothetical prote
8	8	2.0	299	2	T12483	hypothetical prote
9	8	2.0	328	2	JC4800	P2Y6 receptor - hu
10	8	2.0	328	2	I55450	G protein-coupled
11	8	2.0	341	2	T22551	hypothetical prote
12	8	2.0	350	2	A39445	hypothetical prote
13	8	2.0	360	2	A53611	interleukin-8 rece
14	8	2.0	363	2	I48261	interleukin-8 rece
15	8	2.0	386	2	I84612	sensory epithelia
16	8	2.0	386	2	I51667	thrombin receptor
17	8	2.0	420	2	T49675	origin recognition
18	8	2.0	433	2	S64314	probable membrane
19	8	2.0	551	2	T14890	glucose-6-phosphat
20	8	2.0	604	2	C86677	DNA ligase (NAD) (
21	8	2.0	654	2	S67070	GAC1 protein - yea
22	8	2.0	793	2	A30889	integrin beta chai
23	8	2.0	846	2	T00349	Avicelase III - As
24	8	2.0	856	2	T02657	hypothetical prote
25	8	2.0	954	2	G84664	hypothetical prote
26	8	2.0	1732	2	S46404	vitellogenin - yel
27	7	1.8	2139	2	D64055	hypothetical prote
28	7	1.8	63	2	S04922	hypothetical prote
29	7	1.8	73	2	AF1183	homeotic protein H
30	7	1.8	133	2	T42978	hypothetical prote
31	7	1.8	138	2	H97024	uncharacterized sm
32	7	1.8	142	2	S77020	transposase slr080
33	7	1.8	142	2	S77515	transposase 811179
34	7	1.8	150	2	JS0297	hypothetical prote
35	7	1.8	152	2	S35209	infection structur
36	7	1.8	164	2	JC2572	serine proteinase
37	7	1.8	170	2	G90157	hypothetical 18K p
38	7	1.8	197	2	T36584	conserved hypothet
39	7	1.8	201	2	A82235	hypothetical prote
40	7	1.8	210	2	G84751	hypothetical prote
41	7	1.8	214	2	AI1073	probable membrane
42	7	1.8	214	2	A26227	smp protein - Bsch
43	7	1.8	224	2	C82351	DNA repair protein
44	7	1.8	226	2	C70383	conserved hypothet
45	7	1.8	230	2	G82579	conserved hypothet
46	7	1.8	238	2	G64117	F1GF4.1 protein homol
47	7	1.8	239	2	B86346	hypothetical prote
48	7	1.8	254	2	E72335	flagellar biosynth
49	7	1.8	259	2	I40401	hypothetical prote
50	7	1.8	265	2	I40868	hypothetical prote
51	7	1.8	271	2	H82897	hypothetical prote
52	7	1.8	279	2	T20987	replication factor
53	7	1.8	290	2	F90089	probable ABC trans
54	7	1.8	295	2	H95281	conserved hypothet
55	7	1.8	306	2	C95989	conserved hypothet
56	7	1.8	307	2	S04923	homeotic protein H
57	7	1.8	313	2	H36854	hemagglutinin - va
58	7	1.8	314	2	C90256	conserved hypothet
59	7	1.8	315	2	AD1324	transcription repr
60	7	1.8	315	2	AP1695	transcription repr
61	7	1.8	320	2	S18444	G protein-coupled
62	7	1.8	346	2	JC5715	G protein-coupled
63	7	1.8	346	2	JC5716	G protein-coupled
64	7	1.8	349	2	C71470	probable disulfide
65	7	1.8	351	2	JC7096	leukotriene B4 rec
66	7	1.8	352	2	JE0296	thyrotropin releas
67	7	1.8	354	2	B55733	G protein-coupled
68	7	1.8	355	2	AB3008	monooxygenase [imp
69	7	1.8	355	2	H98275	mtaG protein (AF18
70	7	1.8	356	2	AF2137	hypothetical prote
71	7	1.8	359	2	S15403	angiotensin II rec
72	7	1.8	359	2	I51372	angiotensin II rec
73	7	1.8	359	2	I39418	angiotensin II rec
74	7	1.8	359	2	JC1104	angiotensin II rec
75	7	1.8	359	2	S44425	angiotensin II rec
76	7	1.8	359	2	A48857	angiotensin II rec
77	7	1.8	359	2	JH0621	angiotensin II rec
78	7	1.8	359	2	JC1194	angiotensin II rec
79	7	1.8	359	2	A42656	angiotensin II rec
80	7	1.8	359	2	JC2134	angiotensin II rec
81	7	1.8	360	2	A98212	probable fimbrial
82	7	1.8	360	2	A86058	probable fimbrial
83	7	1.8	366	2	F84247	hypothetical prote
84	7	1.8	371	2	G69827	conserved hypothet
85	7	1.8	371	2	B86489	protein T32E20.25
86	7	1.8	378	2	S28789	conserved hypothet
87	7	1.8	382	2	S40693	opsin Rh4 - fruit
88	7	1.8	383	2	A26768	opsin rh3 - fruit
89	7	1.8	383	2	B41544	opsin, R7 photorec
90	7	1.8	384	2	S00516	opsin Rh4 - fruit
91	7	1.8	384	2	I57957	neurokinin 2 recep
92	7	1.8	384	2	S20303	neurokinin 2 recep
93	7	1.8	384	2	I39599	neurokinin 2 recep
94	7	1.8	388	2	A36737	3-amino-5-hydroxyb
95	7	1.8	390	2	A75303	neurokinin 2 recep
96	7	1.8	394	2	B81223	UDP-glucose 4-epim
97	7	1.8	397	2	B81994	conserved hypothet
98	7	1.8	397	1	JQ1059	probable transmemb
99	7	1.8	402	2	I56595	neurokinin 2 recep
100	7	1.8	410	2	A69050	conserved hypothet
101	7	1.8	414	2	C86301	arginine/serine-ri
102	7	1.8	414	2	B84546	probable tetracycl

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: September 16, 2005, 08:17:59 ; Search time 119.5 Seconds
(without alignments)
1288.122 Million cell updates/sec

Title: US-10-643-627-4
Perfect score: 398
Sequence: 1 MNVLSFEQTSVTAEFFISVM..........KHSRKSSSYSSSSTVKTSY 398

Scoring table:
Scoring table: OLIGO
                   Gapop 60.0 , Gapext 60.0
Searched: 2105692 seqs, 386760381 residues
Word size : 0
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :   A_Geneseq_16Dec04:*
    1: geneseqp1980s:*
    2: geneseqp1990s:*
    3: geneseqp2000s:*
    4: geneseqp2001s:*
    5: geneseqp2002s:*
    6: geneseqp2003s:*
    7: geneseqp2003bs:*
    8: geneseqp2004s:*

Post-processing: Listing first 1000 summaries   2105692

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description
1	398	100.0	398	2	Aar66921	Human C14
2	398	100.0	398	2	Aaw01953	Human C14
3	370	93.0	397	3	Aab35641	Human PAR
4	370	93.0	397	5	Aae26678	Human coa
5	370	93.0	397	5	Abg73508	Human par
6	370	93.0	397	7	Ade62812	Human Pro
7	370	93.0	397	8	Ado29311	Human GPC
8	370	93.0	397	8	Ads74020	Human GPC
9	367	92.2	397	6	Adl61221	Human G-p
10	369	92.2	397	6	Abp81907	Human coa
11	269	67.6	397	6	Adk52594	Hematolog
12	269	67.6	397	7	Adn39997	Cancer/an
13	269	67.6	397	8	Adr46675	Cancer-as
14	259	65.1	397	8	Adi28655	Human mod
15	259	65.1	341	8	Adi28654	Human mod
16	259	65.0	355	2	Adi28653	Human mod
17	211	53.0	394	2	Aaw51408	Human pro
18	91	22.9	397	2	Aar66923	Human C14
19	91	22.9	397	2	Aaw01955	Human C14
20	58	14.6	58	8	Abu67239	G-protein
21	58	14.6	58	9	Abp54020	Human pro
22	58	14.6	58	8	Abp54020	Human pro
23	58	14.6	58	8	Ado28760	Proteinas
24	57	14.3	389	8	Ado05264	Human PAR
25	54	13.6	54	8	Adi28666	Human pro

26	37	9.3	397	7	Ade62810	Rat Prote
27	34	8.5	395	2	Aar66920	Murine C1
28	34	8.5	395	2	Aaw01952	Murine C1
29	34	8.5	399	2	Aar66922	Murine C1
30	34	8.5	399	2	Aaw01954	Murine C1
31	34	8.5	399	7	Abr63562	Delayed h
32	34	8.5	399	7	Ado29312	Mouse GPC
33	25	6.3	399	3	Aay45037	Human pro
34	25	6.3	21	7	Aau10420	PAR2 pepd
35	21	5.3	21	7	Aau10421	PAR2 pepd
36	20	5.0	20	8	Abp82705	G protein
37	18	4.5	18	8	Abp82706	G protein
38	18	4.5	18	6	Abp82707	G protein
39	16	4.0	16	8	Abp82708	G protein
40	15	3.8	68	8	Adk35286	Novel hum
41	14	3.5	20	3	Adk35286	Novel hum
42	12	3.0	20	3	Aab36651	Human PAR
43	11	2.8	20	3	Aaw76406	Human PAR
44	13	3.3	13	2	Aab36652	Mouse PAR
45	13	3.3	13	2	Aar66890	Mouse PAR
46	13	3.3	13	2	Aaw01923	Agonist P
47	15	3.8	15	2	Abg35288	C140 rece
48	15	3.8	15	2	Abg35286	Human PAR
49	15	3.8	15	2	Abg35287	Human PAR
50	15	3.8	15	4	Aar27238	Thrombin
51	15	3.8	26	2	Aar27238	Human PAR
52	10	2.5	319	4	Aab82760	Rat G-pro
53	10	2.5	319	8	Ado29401	Mouse GPC
54	10	2.5	371	5	Abg35299	Human PAR
55	10	2.5	371	6	Aaw51406	Human pro
56	10	2.5	374	2	Abg73509	Human pro
57	10	2.5	374	6	Abp81908	Human pro
58	10	2.5	374	7	Adb67661	Human P2R
59	10	2.5	374	8	Ado29313	Human GPC
60	10	2.5	374	8	Adq97469	Human can
61	10	2.5	374	8	Adg39889	Human myo
62	10	2.5	374	8	Ads32990	Proteinas
63	10	2.5	402	2	Abg35298	Human thr
64	10	2.5	425	2	Aar27240	Human thr
65	10	2.5	425	2	Aar60698	Fragment
66	10	2.5	425	2	Aaw51407	Human pro
67	10	2.5	425	8	Aay49570	Human pro
68	10	2.5	425	8	Aae17032	Human thr
69	10	2.5	425	2	Abg35300	Human thr
70	10	2.5	425	8	Aag80697	Human PAR
71	10	2.5	425	2	Abg73511	Human thr
72	10	2.5	425	6	Abr47449	Breast ca
73	10	2.5	425	2	Abp81919	Human thr
74	10	2.5	425	7	Ades8075	Human Pro
75	10	2.5	425	2	Ades8071	Human Pro
76	10	2.5	425	7	Adg99876	Human coa
77	10	2.5	425	8	Adl14208	Novel hum
78	10	2.5	425	8	Adn04016	Antipsori
79	10	2.5	425	8	Ado29309	Human GPC
80	10	2.5	425	8	Adq18985	Human GPC
81	10	2.5	425	8	Adr45608	Human sof
82	10	2.5	426	8	Ads04489	Human G-p
83	10	2.5	426	8	Aay45035	Human pro
84	10	2.5	430	8	Ado29310	Mouse GPC
85	10	2.5	432	7	Ades8073	Rat Prote
86	9	2.5	432	2	Ades8069	Human Pro
87	10	2.5	892	2	Aaw16314	Agonist P
88	9	2.3	12	2	Aar66891	Agonist P
89	9	2.3	12	2	Aaw01924	C140 rece
90	9	2.3	15	5	Abg35284	Human PAR
91	9	2.3	17	2	Aaw76405	Human PAR
92	9	2.3	137	4	Aau41295	Propionib
93	9	2.3	137	4	Aau41295	Propionib
94	8	2.0	8	8	Abm37814	Disease-a
95	8	2.0	11	2	Adp49257	Disease-a
96	8	2.0	11	2	Aar66892	Agonist P
97	8	2.0	15	2	Aaw01925	C140 rece
98	8	2.0	20	2	Abg35283	Human PAR
					Aaw76404	Rat PAR-2